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ATGGACAAAACCTCACACATGTCCACCTTGTCCAGCTCCGGAACCTCTGGGGGGACCGTCA
1 -----+-----+-----+-----+-----+-----+ 60
TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT

a M D K T H T C P P C P A P E L L G G P S -

GTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC
61 -----+-----+-----+-----+-----+-----+ 120
CAGAAGGAGAAGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG

a V F L F P P K P K D T L M I S R T P E V -

ACATGCGTGGTGGTGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
121 -----+-----+-----+-----+-----+-----+ 180
TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC

a T C V V V D V S H E D P E V K F N W Y V -

GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
181 -----+-----+-----+-----+-----+-----+ 240
CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC

a D G V E V H N A K T K P R E E Q Y N S T -

TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
241 -----+-----+-----+-----+-----+-----+ 300
ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCCTCATG

a Y R V V S V L T V L H Q D W L N G K E Y -

AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
301 -----+-----+-----+-----+-----+-----+ 360
TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTGGTAGAGGTTTCGG

a K C K V S N K A L P A P I E K T I S K A -

AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGATGAGCTGACC
361 -----+-----+-----+-----+-----+-----+ 420
TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGG

a K G Q P R E P Q V Y T L P P S R D E L T -

AAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
421 -----+-----+-----+-----+-----+-----+ 480
TTCTTGGTCCAGTCGGACTGGACGGACAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC

a K N Q V S L T C L V K G F Y P S D I A V -

GAGTGGGAGAGCAATGGGCAGCCGAGAACAACACAAAGACCACGCCTCCCGTGTCTGGAC
481 -----+-----+-----+-----+-----+-----+ 540
CTCACCCCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGACCTG

FIG. 1A

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a E W E S N G Q P E N N Y K T T P P V L D -

TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
541 -----+-----+-----+-----+-----+-----+ 600
AGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC

a S D G S F F L Y S K L T V D K S R W Q Q -

GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG
601 -----+-----+-----+-----+-----+-----+ 660
CCCTTGACAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC

a G N V F S C S V M H E A L H N H Y T Q K -

AGCCTCTCCCTGTCTCCGGGTAAA
661 -----+-----+-----+-----+-----+-----+ 684
TCGGAGAGGGACAGAGGCCCATTT

a S L S L S P G K

FIG. 1B

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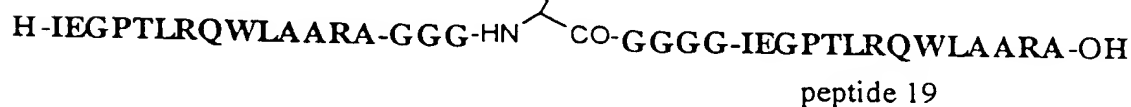
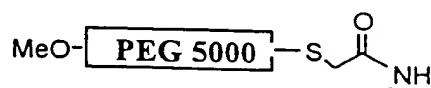
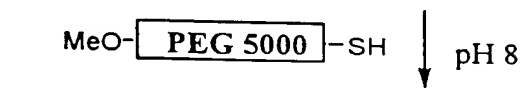
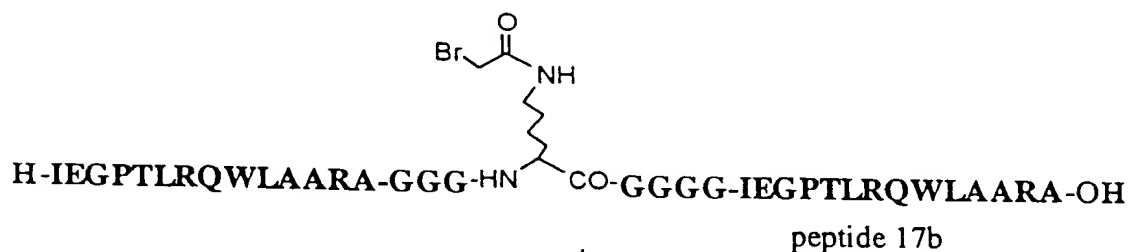
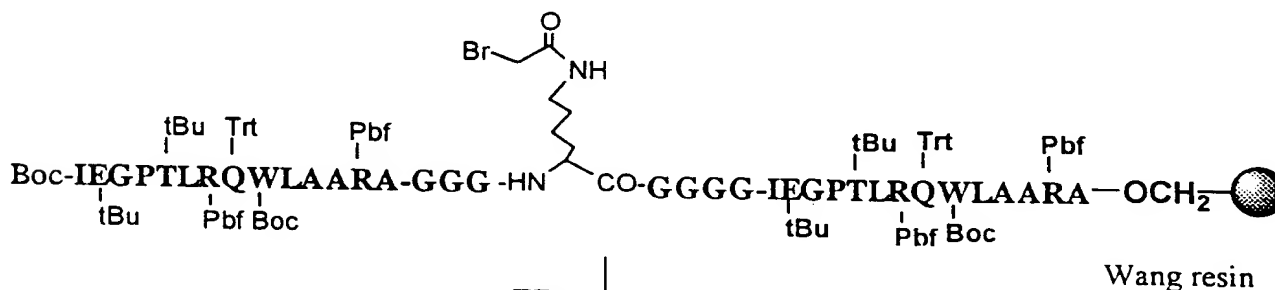
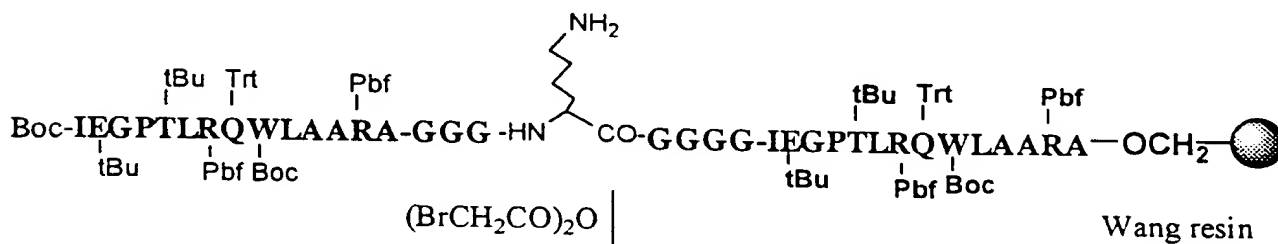
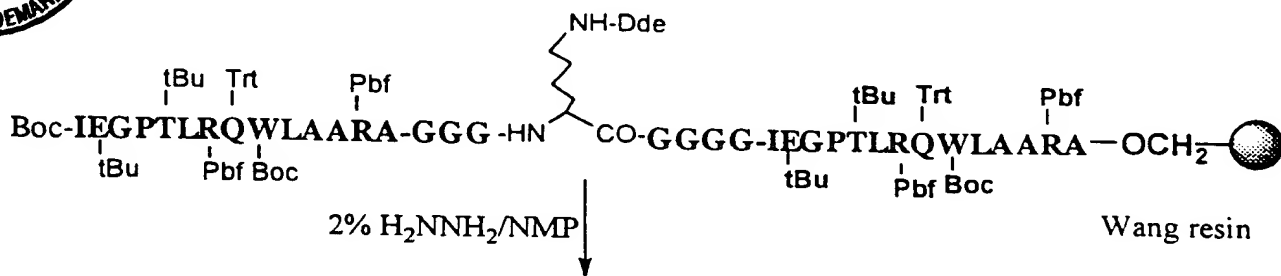


FIG. 2



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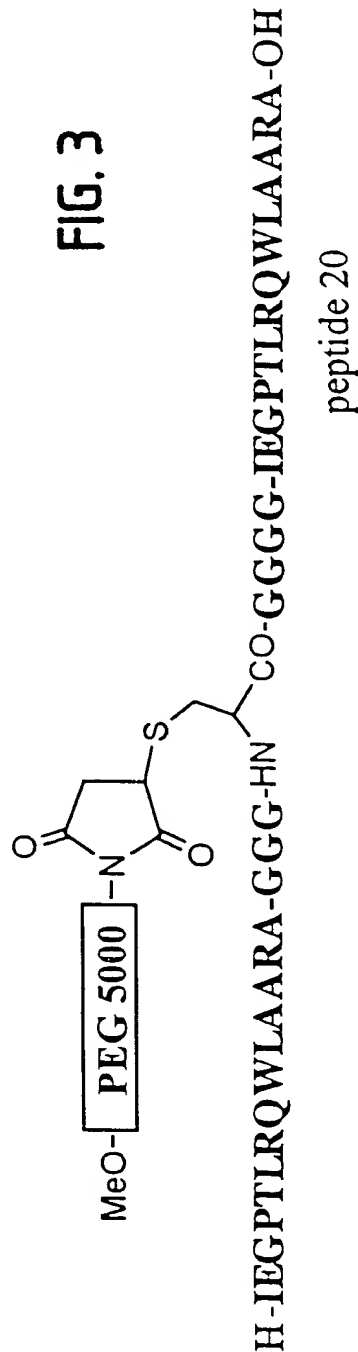
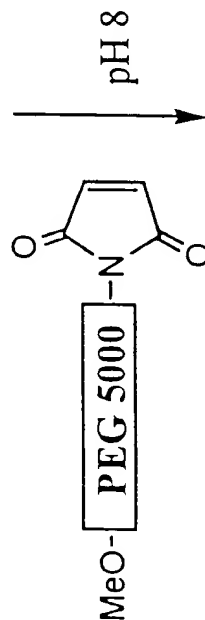
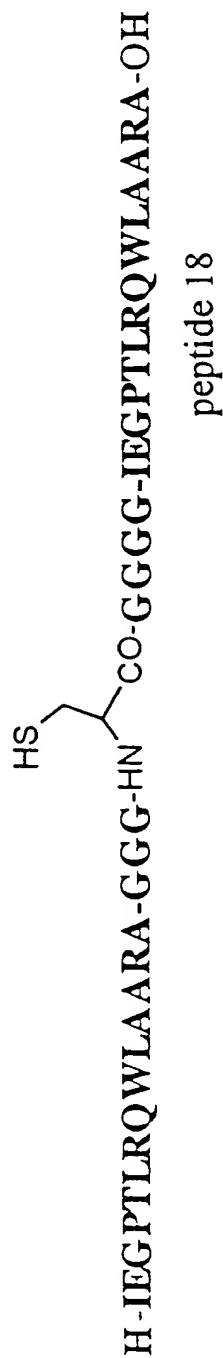
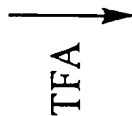
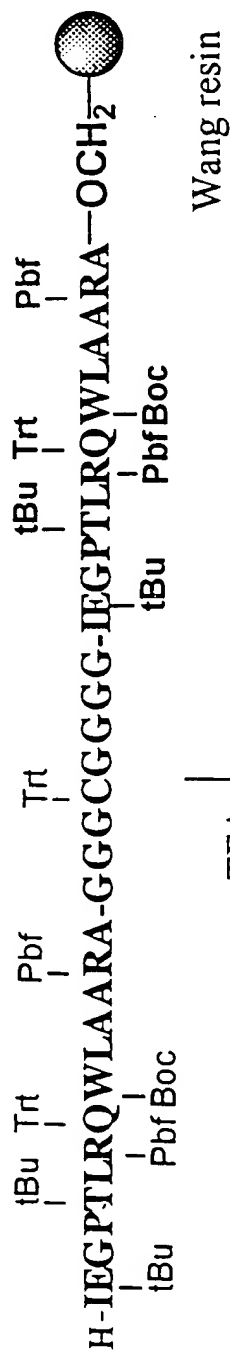


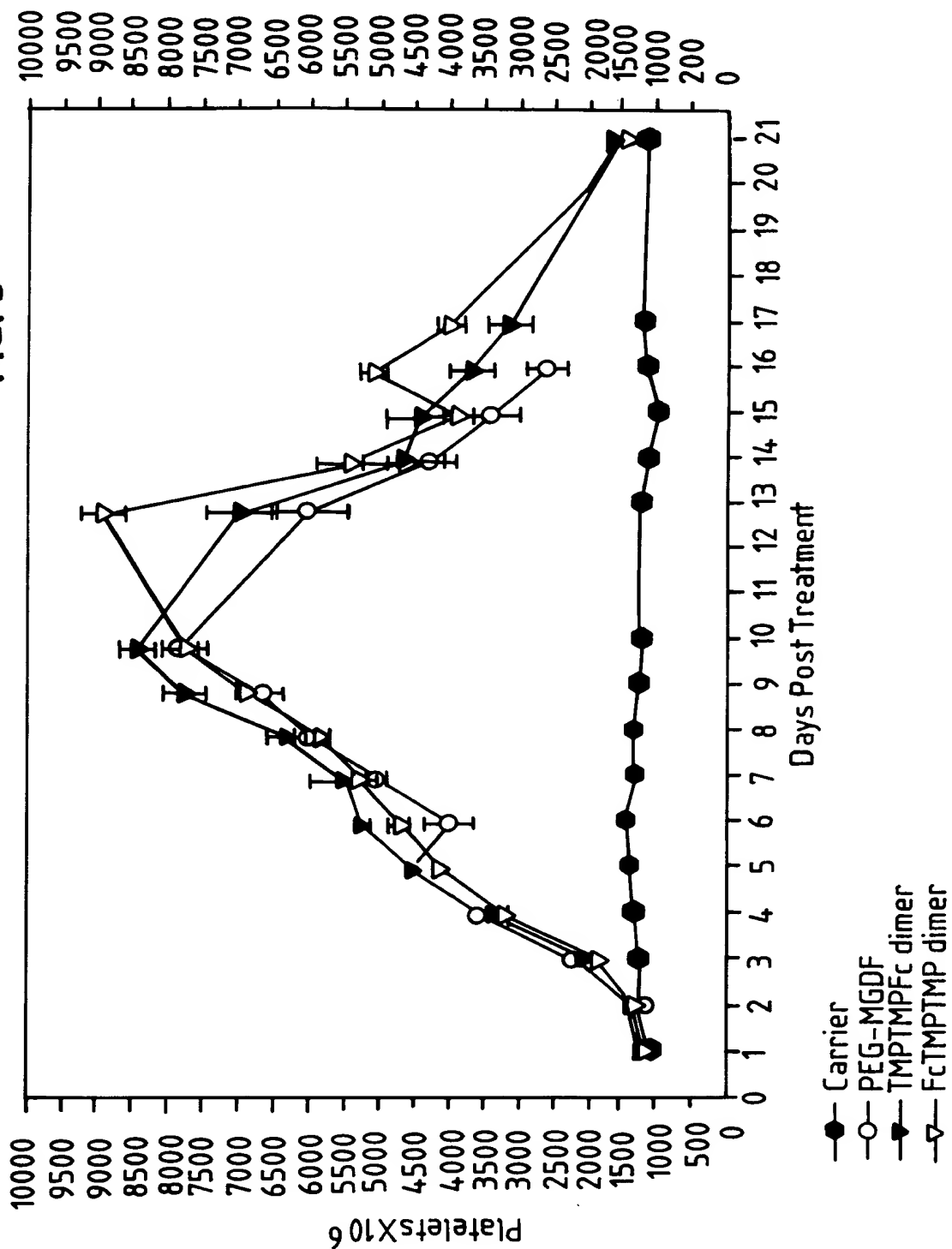
FIG. 3

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FIG. 5





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FIG. 6A



FIG. 6B

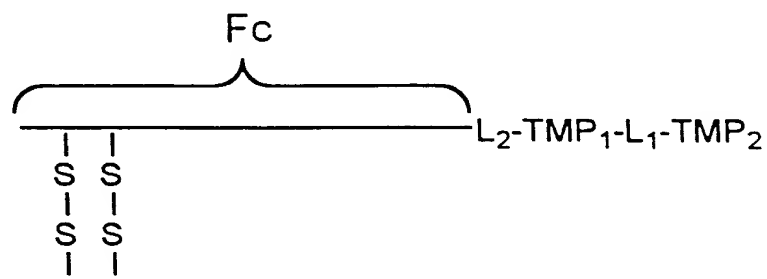


FIG. 6C

